

GTCAATATGCTGTTCAAGTCATGGCAACTGGCAGCAGCCTCCGGGCTCCTGTCTGGAGTC	60
MetLeuPheLysSerTrpGlnLeuAlaAlaAlaSerGlyLeuLeuSerGlyVa	18
CTCGGCATCCCGATGGACACCGGCAGCCACCCCATTTGAGGCTGTGTGATCCCGAAGTGAAG	120
lLeuGlyIleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLy	38
ACTGAGGTCTTCGCTGACTCCCTCCTTGTCTGCAGCAGGCGATGACGACTGGGAGTCACT	180
sThrGluValPheAlaAspSerLeuLeuAlaAlaGlyAspAspSerTrpGluSerPr	58
CCATACAACCTTGCTTTACAGGAATGCCCTGCCAAATCCACCTGTCAAGCAGCCCAAGATG	240
oProTyrAsnLeuLeuTyrArgAsnAlaLeuProIleProProValLysGlnProLysMe	78
ATCATTACCAACCTGTCAACGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCA	300
tIleIleThrAsnProValThrGlyLysAspIleTrpTyrTyrGluIleGluIleLysPr	98
TTTCAGCAAAGGATTTACCCACCTTGCGCCCTGCCACTCTCGTCGGCTACGATGGCGAT	360
oPheGlnGlnArgIleTyrProThrLeuArgProAlaThrLeuValGlyTyrAspGlyMe	118
AGCCCTGGTCTACTTTCAATGTTCCAGAGGAACAGAGACTGTAGTTAGGTTTCATCAAC	420
tSerProGlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAs	138
AATGCCACCGTGGAGAACTCGGTCCATCTGCACGGCTCCCCATCGCGTGGCCCTTTTCGAT	480
nAsnAlaThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaProPheAs	158
GGTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAAGGATTACTACTTTCCCAACTAC	540
pGlyTrpAlaGluAspValThrPheProGlyGluTyrLysAspTyrTyrPheProAsnTy	178
CAATCCGCCCGCCTTCTGTGGTACCATGACCACGCTTTTCATGAAGACTGTGAGAATGCC	600
rGlnSerAlaArgLeuLeuTrpTyrHisAspHisAlaPheMetLysThrAlaGluAsnAl	198
TACTTTGGTCAGGCTGGCGCCTACATTATCAACGACGAGGCTGAGGATGCTCTCGGTCTT	660
aTyrPheGlyGlnAlaGlyAlaTyrIleIleAsnAspGluAlaGluAspAlaLeuGlyLe	218
CCTAGTGGCTATGGCGAGTTCGATATCCCTCTGATCTCGACGGCCAAGTACTATAACGCC	720
uProSerGlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaLysTyrTyrAsnAl	238
GATGGTACCCTGCGTTCGACCGAGGGTGAGGACCAGGACCTGTGGGAGATGTGCATCCAT	780
aAspGlyThrLeuArgSerThrGluGlyGluAspGlnAspLeuTrpGlyAspValIleHi	258
GTCAACGGACAGCCATGGCCTTTCCTTAACGTCCAGCCCCGCAAGTACCGTTTCCGATTC	840
sValAsnGlyGlnProTrpProPheLeuAsnValGlnProArgLysTyrArgPheArgPh	278
CTCAACGCTGCCGTGCTCGTGCTTGGCTCCTCTACCTCGTCAGGACCAGCTCTCCCAAC	900
eLeuAsnAlaAlaValSerArgAlaTrpLeuLeuTyrLeuValThrLeuSerSerProAs	298
GTCAGAATTCCTTTCCAAGTCATTGCCTCTGATGCTGGTCTCCTTCAAGCCCCCGTTTCAG	960
nValArgIleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProValGl	318
ACCTCTAACCTCTACCTTGCTGTTGCCGAGCGTTACGAGATCATTATTGACTTCCACCAAC	1020
nThrSerAsnLeuTyrLeuAlaValAlaGluArgTyrGluIleIleIleAspPheThrAs	338
TTTGCTGGCCAGACTCTTGACCTGCGCAACGTTGCTGAGACCAACGATGTGCGGCGACGAG	1080
nPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaGluThrAsnAspValGlyAspGl	358
GATGAGTACGCTCGCACTCTCGAGGTGATGCGCTTCGTCGTGACGCTCTGGCACGTGTGAG	1140
uAspGluTyrAlaArgThrLeuGluValMetArgPheValValSerSerGlyThrValGl	378

FIG. 1A

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GACAAACAGCCAGGTCCCTCCACTCTCCGTGACGTTTCCTTTCCCTCCTCACAAGGAAGGC	1200
uAspAsnSerGlnValProSerThrLeuArgAspValProPheProProHisLysGluGlu	398
CCC GCCCACAAGCACTTCAAGTTTGAACGCAGCAACGGACACTACCTGATCAACGATGTT	1260
yProAlaAspLysHisPheLysPheGluArgSerAsnGlyHisTyrLeuIleAsnAspVa	418
GGCTTTGCCGATGTCAATGAGCGTGTCTGGCCAAAGCCCGAGCTCGGCACCGTTGAGGTC	1320
lGlyPheAlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValGluVa	438
TGGGAGCTCGAGAACTCCTCTGGAGGCTGGAGCCACCCCGTCCACATTCACCTTGTTGAC	1380
lTrpGluLeuGluAsnSerSerGlyGlyTrpSerHisProValHisIleHisLeuValAs	458
TTCAAGATCCTCAAGCGAACTGGTGGTCGTGGCCAGGTCATGCCCTACGAGTCTGCTGGT	1440
pPheLysIleLeuLysArgThrGlyGlyArgGlyGlnValMetProTyrGluSerAlaGl	478
CTTAAGGATGTCGTCTGGTTGGGCAGGGGTGAGACCCTGACCATCGAGGCCCACTACCAA	1500
yLeuLysAspValValTrpLeuGlyArgGlyGluThrLeuThrIleGluAlaHisTyrGl	498
CCCTGGACTGGAGCTTACATGTGGCACTGTCAACCTCATTCACGAGGATAACGACATG	1560
nProTrpThrGlyAlaTyrMetTrpHisCysHisAsnLeuIleHisGluAspAsnAspMe	518
ATGGCTGTATTCAACGTCACCGCCATGGAGGAGAAGGGATATCTTCAGGAGGACTTCGAG	1620
tMetAlaValPheAsnValThrAlaMetGluGluLysGlyTyrLeuGlnGluAspPheGl	538
GACCCCATGAACCCCAAGTGGCGCGCCGTTCTTACAACCGCAACGACTTCCATGCTCGC	1680
uAspProMetAsnProLysTrpArgAlaValProTyrAsnArgAsnAspPheHisAlaAr	558
GCTGGAAACTTCTCCGCCGAGTCCATCACTGCCCGAGTGCAGGAGCTGGCCGAGCAGGAG	1740
gAlaGlyAsnPheSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGluGlnGl	578
CCGTACAACCGCCTCGATGAGATCCTGGAGGATCTTGGGAATCGAGGAGTAA	1791
uProTyrAsnArgLeuAspGluIleLeuGluAspLeuGlyIleGluGlu	594

FIG. 1B

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CTGGCTAGCC	TCACCTTGSTA	GACAGCCCTG	ACAGCCTCAC	TGGCTGGGGG	TCGAAAGGCC	60
AGTCAATATC	TTGGTCACTG	CTAATAGTTC	CTTGCTACGC	GCAAAAAGCT	CCCTTGCCGAA	120
GGGGCACAGA	CTCATCAAGT	AGACATATAG	GATGCATGTC	TTTCATAGCC	ACAGTTAGGG	180
TGGTGACCTA	CTCAGAGAGG	CCCCGACTTG	GCTGCATACG	ACATGTCCGT	TCCATGCAAC	240
ATGTATGGCG	ACATCGGCGA	TCAGGCACCC	CTGTGCATGCA	GAATAGAACC	CCCGTGGTTT	300
CCTTTTGTTT	CTTTTCCTTT	CTCAACGACG	CGTGAGCGTG	GTTAACTTGA	GCAAGGCCGA	360
TGGGTCTGTT	CACGAGGTTA	CCATCGAACT	CTCTTCTTTT	CCAACTTCGA	CTGCGCCCCC	420
GAGTTTAGCC	CCCATCAACG	CTGTGAAATC	CACCTTCGATA	ATCCCTAGGCT	AGTGCTACTC	480
TTCATAGATT	GCTCCTGATG	GGGCACTTTG	GACCATTTGC	CTTGTTTYCT	CTACCTCGT	540
TCTCTTCCCG	ATCAAGCCCT	TATGCCCGAC	GACAACACCT	CATTGGCCCG	GACCACTTTG	600
AGCGCGCACG	CACCTTCGCG	CCGAAGGAGT	TGATAACACC	CTTCACCCCT	GCCCAATGAT	660
GGAGTTTGG	TCTATTTGTC	ATGATCACTT	CACATTCAC	AGATCACGGA	TCTTGGGAAG	720
GGGTGTGGAA	GCCAGACCCG	CTTGTCCTTG	TTCTTGCGAG	CTCAGGTGAG	CTCTTAGCGG	780
CTATCACAGC	TCAAGATATAT	CAAGTCCCGT	AAAGTCCAGA	CCCTTTTCAT	TGTATGATGC	840
TGCTTAATTT	CGCTATCTCT	TATGCCGTAG	CAGCCGTCTT	GGCTACAAC	GGCTGCCATG	900
GCTGAAGCAT	CGTGAGATCT	ATAAAGGTCT	CCGAATCCTC	GGTGAAGTCA	GAATCGTCTC	960
TCCACACGAG	TCAACAACAA	GCTTCTTTCT	CTTACAGCTT	AGCCTTGAGCA	CATTACACGA	1020
ACTCTTCCCT	TCTTTTCGTC	AATATGCTGT	TCAAGTCACT	GCAACTGGCA	CGAGCCTCCG	1080
GGCTCCTGTC	TGGAGTCCGA	GGCATCCCCA	TGGACACCGG	CAGCCACCCC	ATTAGGCTGT	1140
TGTATCCCCA	AGTGAAGATC	GAGGTCTTCG	CTGACTCCCT	CCCTGCTGCA	GACGCGGATG	1200
ACGACTGGGA	GTCACCTTCA	TACAACCTTC	TTTACAGGTG	AGACACCTGT	CCCACTGTTT	1260
TCTCCCTCGAT	AACATACTCT	TATAGGAATC	CCCTGCCAAT	TCCACCTGTC	AAGCAGCCCA	1320
AGATGTATGT	CTTTGATTTT	CTACGAAGCA	ACTCGGCCCC	GACTAATGTA	TTTATAGGAT	1380
ATTACCAAGC	CTGTACCCGG	CAAGGACATT	TGGTACTATG	AGATCGAGAT	CAAGCCATTT	1440
CAGCAAAAGG	TGAGTTTGCT	CAGAAACCTT	GTGGTAATTA	ATCATTTGTA	CTGACCTTTT	1500
CAGATTTTACC	CCACCTTGCG	CCCTGCCACT	CTCGTCGCT	ACGATTGGCT	GGCCCTCGT	1560
CCTACTTTCA	ATGTTTCCAG	AGGAACAGAG	ACTGTAGTTA	GGTTTCATCA	CAATGCCACC	1620
TGGGAGAACT	CGGTCCATCT	CGACGGCTCC	CCCATCGGCTG	CCCTTTTCGA	TGGTTGGGCT	1680
GAGAGATGTA	GCTTCCCTCG	CGAGTACAA	GATTACTACT	TTCCCAACTA	CCAATCCGCG	1740
CGCTCTCTGT	GGTACCATGA	CACACGCTTT	ATGAAGGTAT	GCTCAGAGCC	TTTATCTTTT	1800
TGGGTACTCT	TTGGCTAAAC	AACCTCTTTT	CGTAGACTGC	TGAGAAATGCC	TACTTTTGGT	1860
AGGCTGCGCG	CTACATTATC	AACGACGAGG	CTGAGGATGC	TCTCGGCTCT	CTCATGTGGCT	1920
ATGGCGAGTT	CGATATCCCT	CTGATCTCGA	GGGCCAAGTA	CTATAACGCC	GATGTGATCC	1980
TGCGTTTCGAC	CGAGGGGTGAG	GACCAAGGAC	TGTGCGGAGA	TGTCTATCCAT	GTCAACGGAC	2040
AGCCATGGCC	TTTCTTTAAC	GTCCAGCCCC	GCAAGTACCG	TTTCCGATTC	CTCAACGCTG	2100
CCGTGCTCTG	TGCTTGGCTC	CTCTAACCTG	TCTAGGACCT	CTCTCCCAAT	GCTCTCAGCA	2160
CTTTCCAAAT	CATTGCCCTT	GATGCTGGTC	TCCTTCAAGC	CCCGCTTCAG	ACCTCTAAAC	2220
TCTACCTTGC	TGTTGCCGAG	CGTTACGAGA	TCATTATTGG	TATGCCCCCT	GCTCTCAGCA	2280
ATGATCTCAAG	AACCTTAAGA	CTAACACTTG	TAGACTTCCAC	CAACTTTGCT	GGCCAGCACT	2340
TTGACCTCGG	CAACGTTGCT	GAGACCAACG	ATGTCGCGCA	CGAGGATGAG	TACAGCTCGCA	2400
CTCTCGAGGT	GATCGGCTCT	GTCGTCAGCT	CTGGCAGCTG	TGAGGACAA	AGCCAGGTCC	2460
CCTCCACTCT	CCGTGACGTT	CCTTTCCCTC	GATCAACGGA	AGGCCCCGCG	GACAAGCACT	2520
TCAAGTTTGA	ACGCGACAAC	GGACACTACC	GATCAACGGA	TGTTGGGCTT	GGCGATGTCA	2580
ATGAGCGTGT	CTTGCGGCA	CCCGAGCTCG	GCCAGCTTGA	GGTCTGGGAG	CTCGAGAAT	2640
CCTCTGGAGG	CTGAGGCCAC	CCCGTCCACA	TTCACTTTGT	TGACTTCAA	ATCCCTCAAG	2700
GAACTGCTGG	TCGTGGCCAG	GTCATGCCCT	ACGAGTCTGT	TGGCTTTAAG	GATGTCGCT	2760
GGTTGGGCGG	GGGTGAGACC	CTGACCATCG	AGGCCCACT	CCAACTTGG	ACTGAGGCTT	2820
ACATGTGGCA	CTGTCAACAC	CTCATTCAG	AGGATAACGA	CATGATGGCT	GTTATCAACG	2880
TCAACGCCAT	GGAGGCGAAG	GGATATCTTC	AGGAGGACTT	CGAGGACCCC	ATGAACCCCA	2940
AGTCGCGCGC	CGTTCCTTAC	ACCTTCCATG	TCGCGCTGGA	AACCTTCTCG	GAACCTCTCG	3000
CCGAGTCCAT	CACCTGCCCG	GTCGAGGAGC	TGGCCGAGCA	GAGAGCCGAT	AACCCGCTCG	3060
ATAGAGTCTT	GGAGGATCTT	GGAAATCGAG	AGTAAACCCC	GAGCCACAAG	CTCTCAACT	3120
GCTTTTGAAG	TTAAGACGAG	GCTCTTGGTG	CGTATTTCTT	TCTTCCCTAT	GGGGAACTCC	3180
GCTGTGCACT	CGCATGTGAA	GGACCATCAC	AAAGCAACCT	ATATATTTGA	CTCACCACTG	3240
TCAATTACCCG	CCACTTGTAC	CTATTGCTAT	CTTTGTTCAA	CTTTTCTAGT	GGCGAGATGT	3300
CACTAGTCAA	GAAACGCCCA	TAGGGCTATC	GTCTAACTG	AACATTTGTG	TGCTTCTGTA	3360
CTGCGAGTGA	ATGTCATATG	TGATGAGACA	CGTAAATATC	GGTATATCTT	TTCTTAGGAC	3420
TACAGGATCA	GTCTTCTATG	AGATTACATC	CAGTAAATGT	TTGTTCATGT	GATCTTAGCT	3480
AAGGTTGAGA	ATGCATCAGA	GGGAATCAT	TGATGCTCTT	AGCTCGTAT	ACCGATGTAA	3540
GACAAAGTTAG	GTAAGTTGCT	TGGTATCCGA	AAATGACTCA	GGCTCCCTCA	TTAGGTTGCA	3600
TGTGAAAAAC	TTACGCAACT	CATGGGTGTT	GGGACCAAA	CATCCATACC	TGATTTTGTAT	3660
AACGTACCTG	GGTCAAT					3677

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1 .....MFKHTLGAAALSLLFNSNAVQA.SPVPETSPATGHLFKRV 39
      |           |           |           |
1  MLFKSQWLAASAGLLSGVLGIPMDTGSHP IEAVDPEVKKTEVFADSLAAA 50
      |           |           |           |           |
40 AQISPOYPMFTV....PLPIPPVKQPRLTVTNPVNGQEIWYVEIEKPF 85
      |           |           |           |           |
51 GDDDWESPYPNLLYRNALPIPPVKQPKMIITNPVTGKDIWYVEIEIKPFQ 100
      |           |           |           |           |
86 HQVYPDLGSADLVGYDGMSPGPTFQVPRGVETVVRFINNAEAPNSVHLHG 135
      |           |           |           |           |
101 QRIYPTLRPATLVGYDGMSPGPTFNVPRGTETVVRFINNATVENSVHLHG 150
      |           |           |           |           |
136 SFSRAAFDGAEDITEPGSFKDYYPNQRSARTLWYHDHAMHITAENAYR 185
      |           |           |           |           |
151 SPSRAPFDGAEDVTFPGGEYKDYFFPNYQSARLLWYHDHAFMKTAENAYF 200
      |           |           |           |           |
186 GQAGLYMLTDPADALNLPDSGYGEFDIPMILTSKQYTANGNLVTTNGELN 235
      |           |           |           |           |
201 GQAGAYIINDEAEDALGLPSGYGEFDIPLILTAKYYNADGTLRSTEGEDQ 250
      |           |           |           |           |
236 SFWGDVIVHVGQWPWPFKNVEPRKYRFRFLDAAVSRSGLYFADTDAIDTR 285
      |           |           |           |           |
251 DLWGDVIVHVGQWPWFLNVQPRKYRFRFLNAAVSRALLYLVRTSSPNVR 300
      |           |           |           |           |
286 LPFKVIASDSGLLEHPADTSLLYISMAERYEVVDFSDYAGKTIELRNLG 335
      |           |           |           |           |
301 IPFQVIASDAGLLQAPVQTSNLYLAVAERYEIIIDFTNFAGQTLDLRNV. 349
      |           |           |           |           |
336 GSIGGIGTDDTDYDNTDKVMRFVVAADTTQPDTSVVPANLRDVFFPSPTTN 385
      |           |           |           |           |
350 AETNDVGDEDEYARTLEVMRFFVSSGTVE.DNSQVPSTLRDVFFPPHKEG 398
      |           |           |           |           |
386 .TPRQFRFRGRTGPTWTINGVAFADVQNRLLANVPVGTVERWELINAGNW 434
      |           |           |           |           |
399 PADKHFKFERSNGHYLINDVGFDVNERVLAKPELGTVEVWELNSSGGW 448
      |           |           |           |           |
435 THPIHIHLVDFKVISRTSGNNARTVMPIYES.GLKDVVWLGRRETVVVEAH 483
      |           |           |           |           |
449 SHPVHIHLVDFKILKRTGGRG..QVMPYESAGLKDVVWLGRGETLTIEAH 496
      |           |           |           |           |
484 YAPFPGVYMFHCHNLIHEDHDMMAAFNATVLPDYGYNAVTFVDPMEELWQ 533
      |           |           |           |           |
497 YQPWIGAYMWHCHNLIHEDNDMMAVFNVTAMEEKGYLQEDFEDPMNPKWR 546
      |           |           |           |           |
534 ARPYELGEFAQSQGSQFSVQAVTERIQTMAEYRFPYAAADE..... 572
      |           |           |           |           |
547 AVPYNRNDFHARAGNFSAESITARVQELAEQEPYNRLDEILEDLGIEE 594

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FIG._3

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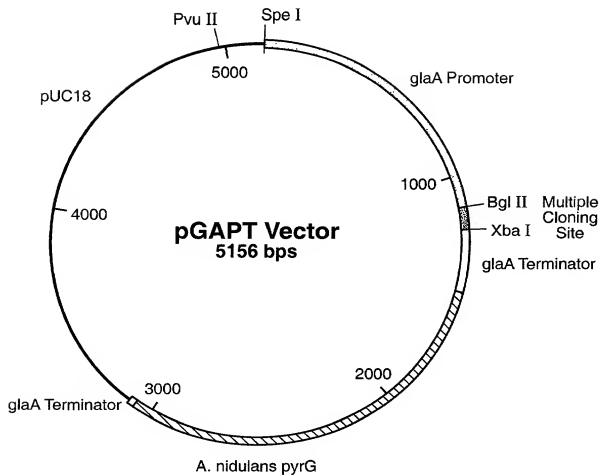


FIG. 4

AGATCTAATA	TGCTGTTCAA	GTCAATGGCAA	CTGGCAGCAG	CCTCCGGGCT	CCTGTCTGGA	60
GTCTTCGGCA	TCCCGATGGA	CACCGGCAGC	CACCCCATTG	AGGCTGTGTA	TCCCGAAGTG	120
AAGACTGAGG	TCTTCGCTGA	CTCCCTCCTT	GCTGCAGCAG	GCGATGACGA	CTGGGAGTCA	180
CCTCCATACA	ACTTGCTTTA	CAGGTGAGAC	ACCTGTCCCA	CCTGTTTTCC	CTCGATAACT	240
AACCTCTATA	GGAATGCCCT	GCCAATTCCA	CCTGTCAAGC	AGCCCAAGAT	GTATGTCTTT	300
GATTTTCTAC	GAAGCAACTC	GGCCCCGACT	AATGTATTCT	AGGATCATT	CCAACCCCTG	360
CACCGGCAAG	GACATTGGGT	ACTATGAGAT	CGAGATCAAG	CCATTTTCAG	AAAGGGTGAG	420
TTTGCTCAGA	AACCTTGTTG	TAATTAATCA	TTGTTACTGA	CCCTTTCAGA	TTTACCCAC	480
CTTGCGCCCT	GCCACTCTCG	TCGGCTACGA	TGGCATGAGC	CCTGGTCCTA	CTTTCAATGT	540
TCCCAGAGGA	ACAGAGACTG	TAGTTAGGTT	CATCAACAAT	GCCACCGTGG	AGAACTCGGT	600
CCATCTGCAC	GGCTCCCAT	CGCGTGCCCC	TTTCGATGGT	TGGGTGAAG	ATGTGACCTT	660
CCCTGGCGAG	TACAAGGATT	ACTACTTTCC	CAACTACCAA	TCCGCCCGCC	TTCTGTGTTA	720
CCATGACCAC	GCTTTTCATGA	AGGTATGCTA	CGAGCCTTTA	TCTTTCTTGG	CTACCTTTGG	780
CTAACCAACT	TCTTTTCGTA	AATGCTGAG	GACTGCTACT	TTGGTCAGGC	TGGCGCCTAC	840
ATTATCAACG	ACGAGGCTGA	GGATGCTCTC	GGTCTTCTTA	GTGGCTATGG	CGAGTTCGAT	900
ATCCCTCTGA	TCCTGACGGC	CAAGTACTAT	AACGCCGATG	GTACCTCGCG	TTGACCGGAG	960
GGTGAGGACC	AGGACCTGTG	GGGAGATGTC	ATCCATGTCA	ACGGACAGCC	ATGGCCCTTC	1020
CTTAACGTTC	AGCCCCGCAA	GTACCCTTTC	CGATTCCCTCA	ACGCTGCCGT	GTCTCGTGCT	1080
TGGCTCCTCT	ACCTCGTCA	GACCAGCTCT	CCCAACGTCA	GAATTCCTTT	CCAAGTCATT	1140
GCCTCTGATG	CTGGTCTCCT	TCAAGCCCCC	GTTTCAGACCT	CTAACCTCTA	CCTTGCTGTT	1200
GCCGAGCGTT	ACGAGATCAT	TATTGGTATG	CCCTCCCTCT	TCACGAATGA	GTCAAGAACT	1260
CTAAGACTAA	CACCTGTAGA	CTTCACCAAC	TTTGCTGGCC	AGACTCTTGA	CCTGCGCAAC	1320
GTTGCTGAGA	CCAACGATGT	CGGCGACGAG	GATGAGTACG	CTCGCACTCT	CGAGGTGATG	1380
CGCTTCGTCG	TCAGCTCTGG	CACGTGTGAG	GACAACAGCC	AGGTCCCCCTC	CACTCTCCGT	1440
GACGTTCCCT	TCCCTCCTCA	CAAGGAAGGC	CCCGCCGACA	AGCACTTCAA	GTTTGAACGC	1500
AGCAACGGAC	ACTACCTGAT	CAACGATGTT	GGCTTTGCCG	ATGTCAATGA	GCGTGTCTCG	1560
GCCAAGCCCG	AGCTCGGCAC	CGTTGAGGTC	TGGGAGCTCG	AGAACTCCTC	TGGAGGCTGG	1620
AGCCACCCCG	TCCACATTCA	CCTTGTTGAC	TTCAAGATCC	TCAAGCGAAC	TGGTGGTCTG	1680
GGCCAGGTCA	TGCCCTACGA	GTCTGCTGGT	CTTAAGGATG	TCGCTCTGTT	GGGCAGGGGT	1740
GAGACCTTGA	CCATCGAGGC	CCACTACCAA	CCCTGGACTG	GAGCTTACAT	GTGGCACTGT	1800
CACAACCTCA	TTACGAGGA	TAACGACATG	ATGGCTGTAT	TCAACGTAC	CGCCATGGAG	1860
GAGAAGGGAT	ATCTTCAGGA	GGACTTCGAG	GACCCCATGA	ACCCCAAGTG	GCGCGCCGTT	1920
CCTTACAACC	GCAACGACTT	CCATGCTCGC	CTCTGCGCGA	TCTCTGCGCA	GTCCATCACT	1980
GCCCGAGTGC	AGGAGCTGGC	CGAGCAGGAG	CCGTACAACC	GCCTCGATGA	GATCTTGGAG	2040
GATCTTGGAA	TCGAGGAGTA	GTCTAGA				2067

FIG._5

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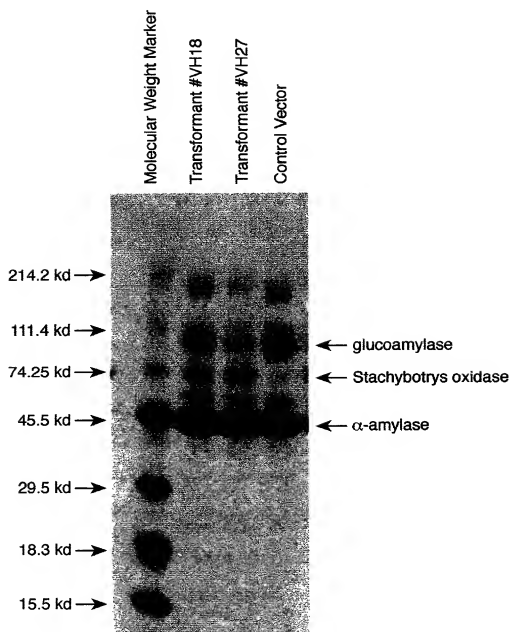


FIG._6